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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER Sarada Prasad

ART UNIT	PAPER
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1646

8

DATE MAILED:

**Please find below and/or attached an Office communication concerning this application or proceeding.**

Commissioner of Patents

**Sequence Rules**

The reply filed on 8/16/01 (Paper No. 7) is not fully responsive to the prior Office Action because of the following omission(s) or matter(s):

See attached Raw sequence listing -error report.

Since the above-mentioned reply appears to be bona fide, applicant is given ONE (1) MONTH or THIRTY (30) DAYS from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a)

**Advisory Information**

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sarada C Prasad whose telephone number is 703-305-1009. The examiner can normally be reached Monday – Friday from 8.00 AM to 4.30 PM (Eastern time).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne Eyler, can be reached on (703) 308-6564. The fax phone number for the organization where this application or proceeding is assigned is 703-308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Sarada Prasad, Ph.D.  
Examiner  
Art Unit 1646  
September 10, 2001

*Prema Mertz*  
PREMA MERTZ  
PRIMARY EXAMINER

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

09/508,570

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2        Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3   ✓   Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4        Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5        Variable Length  
Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6        PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7        Skipped Sequences  
    (OLD RULES)  
Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8        Skipped Sequences  
    (NEW RULES)  
Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9   ✓   Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10        Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11        Use of <220>  
Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown.". Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12        PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13        Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/508,510

DATE: 09/06/2001

TIME: 17:52:33

Input Set : A:\56400002-sequence.txt

Output Set: N:\CRF3\09062001\I508510.raw

pp 1-3  
Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Tschope, Michael;  
4 Siklosi, Thomas;  
5 Schroeder, Peter; and  
6 Hofer, Hans.  
8 <120> TITLE OF INVENTION: Liquid Interferon-BETA Formulations  
10 <130> FILE REFERENCE: 17150P US WO (DR)  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/508,510  
13 <141> CURRENT FILING DATE: 2000-05-26  
15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06065 and EP 97 116 562.6  
W--> 16 <151> PRIOR FILING DATE: 1998-09-23 (PCT/EP98/06065) and 1997-09-23 (EP 97 116 562.6)  
18 <160> NUMBER OF SEQ ID NOS: 14  
20 <170> SOFTWARE: PatentIn Ver. 2.1

*list these  
as separate  
(1507 and 1517)*

## ERRORED SEQUENCES

22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 7  
24 <212> TYPE: PRT  
25 <213> ORGANISM: Homo sapiens  
27 <400> SEQUENCE: 1  
28 Glu Asp Phe Thr Arg Gly Lys  
E--> 29 1 5  
33 <210> SEQ ID NO: 2  
34 <211> LENGTH: 6  
35 <212> TYPE: PRT  
36 <213> ORGANISM: Homo sapiens  
38 <400> SEQUENCE: 2  
39 Thr Val Leu Glu Glu Lys  
E--> 40 1 5  
44 <210> SEQ ID NO: 3  
45 <211> LENGTH: 7  
46 <212> TYPE: PRT  
47 <213> ORGANISM: Homo sapiens  
49 <400> SEQUENCE: 3  
50 Gln Leu Gln Gln Phe Gln Lys  
E--> 51 1 5  
55 <210> SEQ ID NO: 4  
56 <211> LENGTH: 8  
57 <212> TYPE: PRT  
58 <213> ORGANISM: Homo sapiens  
60 <400> SEQUENCE: 4  
E--> 61 Leu Xaa Ser Ser Leu His Leu Lys  
E--> 62 1 5  
66 <210> SEQ ID NO: 5  
67 <211> LENGTH: 8  
68 <212> TYPE: PRT

*misaligned amino acid numbers  
(global env) see item 3  
on Env*

*summary sheet*

*same env*

*see item 9 on Env summary sheet*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/508,510

DATE: 09/06/2001

TIME: 17:52:33

Input Set : A:\56400002-sequence.txt

Output Set: N:\CRF3\09062001\I508510.raw

69 <213> ORGANISM: Homo sapiens  
 71 <400> SEQUENCE: 5  
 72 Leu Met Ser Ser Leu His Leu Lys  
 E--> 73 1 5  
 75 <210> SEQ ID NO: 6  
 76 <211> LENGTH: 12  
 77 <212> TYPE: PRT  
 78 <213> ORGANISM: Homo sapiens  
 80 <400> SEQUENCE: 6  
 E--> 81 Asp Arg Xaa Asn Phe Asp Ile Pro Glu Glu Ile Lys 10  
 E--> 82 1 5  
 86 <210> SEQ ID NO: 7  
 87 <211> LENGTH: 11  
 88 <212> TYPE: PRT  
 89 <213> ORGANISM: Homo sapiens  
 91 <400> SEQUENCE: 7  
 92 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys 10  
 E--> 93 1 5  
 97 <210> SEQ ID NO: 8  
 98 <211> LENGTH: 12  
 99 <212> TYPE: PRT  
 100 <213> ORGANISM: Homo sapiens  
 102 <400> SEQUENCE: 8  
 103 Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys 10  
 E--> 104 1 5  
 108 <210> SEQ ID NO: 9  
 109 <211> LENGTH: 14  
 110 <212> TYPE: PRT  
 111 <213> ORGANISM: Homo sapiens  
 E--> 112 <400> SEQUENCE: 9  
 113 Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys 10  
 E--> 114 1 5  
 118 <210> SEQ ID NO: 10  
 119 <211> LENGTH: 19  
 120 <212> TYPE: PRT  
 121 <213> ORGANISM: Homo sapiens  
 123 <400> SEQUENCE: 10  
 E--> 124 Xaa Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
 E--> 125 1 5 10 15  
 127 Cys Gln Lys  
 132 <210> SEQ ID NO: 11  
 133 <211> LENGTH: 19  
 134 <212> TYPE: PRT  
 135 <213> ORGANISM: Homo sapiens  
 137 <400> SEQUENCE: 11  
 138 Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
 E--> 139 1 5 10 15  
 141 Cys Gln Lys  
 146 <210> SEQ ID NO: 12

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/508,510

DATE: 09/06/2001

TIME: 17:52:33

Input Set : A:\56400002-sequence.txt

Output Set: N:\CRF3\09062001\I508510.raw

147 <211> LENGTH: 30  
 148 <212> TYPE: PRT  
 149 <213> ORGANISM: Homo sapiens  
 151 <400> SEQUENCE: 12  
 152 Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg  
 E--> 153 1 5 10 15  
 155 Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn  
 E--> 156 20 25 30  
 160 <210> SEQ ID NO: 13  
 161 <211> LENGTH: 47  
 162 <212> TYPE: PRT  
 163 <213> ORGANISM: Homo sapiens  
 165 <400> SEQUENCE: 13  
 E--> 166 Glu Asp Ala Ala Leu Thr Ile Tyr Glu Xaa Leu Gln Asn Ile Phe Ala  
 E--> 167 1 5 10 15  
 169 Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val  
 E--> 170 20 25 30  
 172 Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys  
 E--> 173 35 40 45  
 177 <210> SEQ ID NO: 14  
 178 <211> LENGTH: 47  
 179 <212> TYPE: PRT  
 180 <213> ORGANISM: Homo sapiens  
 182 <400> SEQUENCE: 14  
 183 Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala  
 E--> 184 1 5 10 15  
 186 Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val  
 E--> 187 20 25 30  
 189 Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys  
 E--> 190 35 40 45  
 E--> 194 VI  
 196 I  
 E--> 198 VI  
 200 I  
 E--> 202 IV  
 E--> 204 I

*len 9*

*delete at end of file*

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/508,510

DATE: 09/06/2001

TIME: 17:52:34

Input Set : A:\56400002-sequence.txt

Output Set: N:\CRF3\09062001\I508510.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:29 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
L:40 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
L:51 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3  
L:61 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4  
M:332 Repeated in SeqNo=4  
L:73 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5  
L:81 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6  
M:332 Repeated in SeqNo=6  
L:93 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:104 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
L:112 M:283 W: Missing Blank Line separator, <400> field identifier  
L:114 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9  
L:124 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10  
M:332 Repeated in SeqNo=10  
L:139 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11  
L:153 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12  
M:332 Repeated in SeqNo=12  
L:166 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13  
M:332 Repeated in SeqNo=13  
L:184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14  
M:332 Repeated in SeqNo=14  
L:194 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:194 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:198 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:198 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:202 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:202 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:204 M:252 E: No. of Seq. differs, <211>LENGTH:Input:47 Found:50 SEQ:14